Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Period: \_\_\_\_\_

**Unit 8 Notes, Part A – Classification of Organisms**

Ms. Ottolini, AP Biology, 2012-2013

**Phylogenies show evolutionary relationships**

1. Phylogeny = evolutionary history of a species or a group of related species ; uses evidence from systematics (a scientific discipline focused on determining evolutionary relationships between organisms based on fossil, morphology/anatomy, and molecular evidence)
2. Taxonomy = using phylogeny to group organisms into categories

* Established by Carolus Linnaeus
* Derived the system of binomial nomenclature, a two-part naming system that includes the “genus” name (group of similar species) and “species identifier” (ex: *Canis familiaris –* Common dog)
* Scientific names are written in Latin to ensure that names are the same anywhere in the world

Ex: Common Names for Bluegill = bream, sunperch, blue sunfish, copperbelly ; Scientific Name = *Lepomis macrochirus*

* The hierarchical classification of organisms consists of the following levels, starting with the most general/inclusive level: domain, kingdom, phylum. class, order, family, genus, and species.
* Each group within any level listed above is called a taxon

**Evidence for systematics**

1. Scientists studying systematics use morphological and molecular data to infer phylogeny (evolutionary history)
2. Morphological data

* Homologous structures = similarities due to shared ancestry (having a common ancestor) ; result from divergent evolution – ex: the bones of a whale’s flipper and a tiger’s paw
* Analogous structures = similarities due to similar environmental requirements and similar functions ; these similarities do not indicate shared ancestry ; result from convergent evolution – ex: the wings of a butterfly and a bat

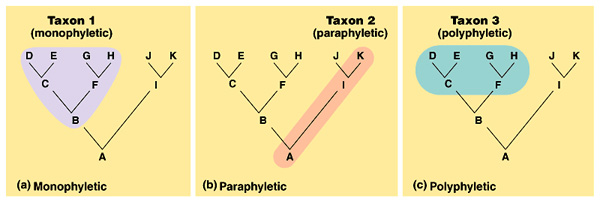
1. Molecular data

* DNA and amino acid sequences
* The more alike the DNA or amino acid sequences of two organisms, the more closely related they are evolutionarily

**Diagramming phylogenies**

1. A cladogram depicts patterns of shared traits (either morphological or molecular) among groups of organisms
2. A clade (found within a cladogram) is a group of species that includes an ancestral species and all its descendants

A clade is considered monophyletic, not paraphyletic or polyphyletic (check out the diagrams below to understand why!)



* Monophyletic Group = consists of an ancestral species and ALL of its descendants
* Paraphyletic Group = consists of an ancestral species and some of its descendants but not all of its descendants
* Polyphyletic Group = consists of descendants of two or more ancestors

1. Shared DERIVED traits/characters are used to construct cladograms… these are traits that are shared among members of a clade and result from recent common ancestry… shared derived traits are also called synapomorphies and result from homologies, not analogies

***For example, consider a jellyfish, starfish, and a human; which two are most closely***

***related?***

The jellyfish and starfish live in the water, have radial symmetry, and are invertebrates,

so you might suppose that they belong together in a group. This would not reflect

evolutionary relationships, however, since the starfish and human are actually more

closely related. In the example above, all three characteristics are believed to have been

present in the common ancestor of all animals, and so are trivial for determining

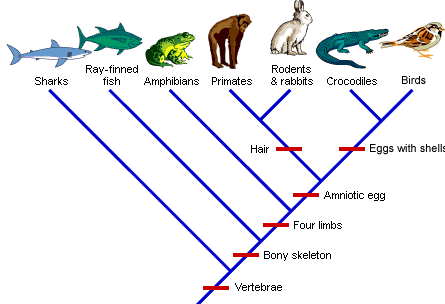
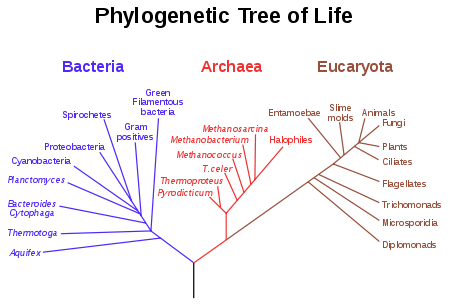
relationships, since all three organisms in question belong to the group "animals". While

humans are different from the other two organisms, they differ only in characteristics

which arose newly in an ancestor which is not shared with the other two.

1. Each branch on a cladogram represents a new homology (shared trait) unique to members of that clade
2. Each point of branching on a cladogram is called a node
3. Phylogenetic trees are cladograms that show the relative amount of change in traits after a branching point (ex: eukaryotic organisms are more closely related to the archaea, a group of single celled prokaryotes living in extreme environments, than they are to true bacteria… however, they have very different traits from the archaea, which is shown by the extremely long branch connecting the common ancestor of eucaryota and archaea)

**Cladogram**

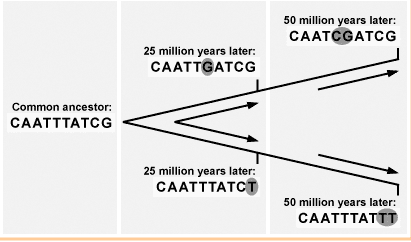
 

**Determining the timeline of evolution**

1. The rate of evolution/change of DNA sequences varies from one part of the genetic code to another

* DNA that codes for ribosomal RNA changes relatively slowly and is useful for investigating relationships between taxa that diverged (branched off) hundreds of millions of years ago
* DNA that codes for mitochondrial DNA evolves rapidly and can be used to explore recent evolutionary events
* Molecular clocks are methods used to measure the absolute time of evolutionary change based on the observation that some genes and other regions of the genome appear to evolve at constant rates

Ex: the gene that codes for the protein alpha-globin (a component of hemoglobin) experiences base changes at a rate of .56 changes per base pair per billion year

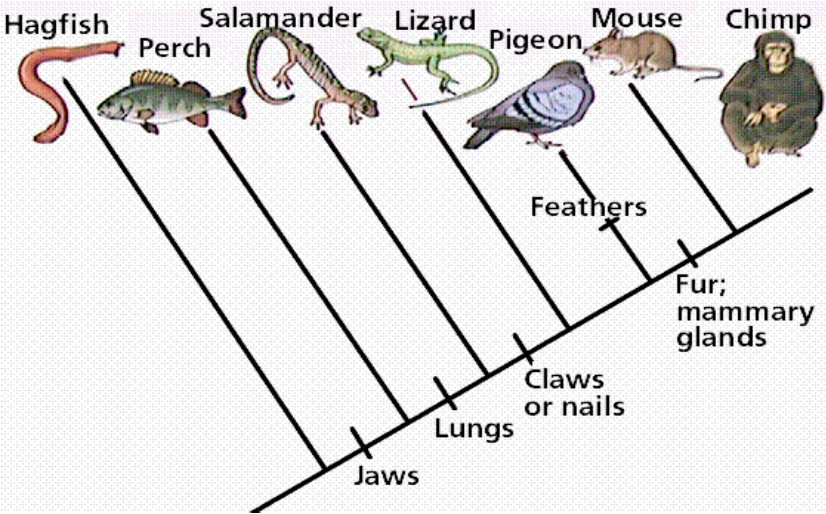


***Sequence serving as a molecular clock (one base change every 25 million years)***

**Follow-Up Questions**

***Part 1: Analyzing a Cladogram***

Analyze the cladogram below by answering the associated questions.



1. After which animals did mammary glands develop?\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

2. What animal does not have jaws? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

3. Which animals have lungs? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

4. Which animals are probably predators? \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

5. After which animal did protection from the elements arise?\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

***Part 2: Creating a Cladogram***

To make a cladogram, you must first look at the animals you are studying and establish characteristics that they share and ones that are unique to each group. For the animals on the table, indicate whether the characteristic is present or not by placing a checkmark in boxes for organisms that possess a given trait. Based on that chart, create a cladogram

**Step 1: Creating a Table of Shared Characteristics**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Cells | Backbone | Legs | Hair | Opposable Thumbs |
| Slug |  |  |  |  |  |
| Catfish |  |  |  |  |  |
| Frog |  |  |  |  |  |
| Tiger |  |  |  |  |  |
| Human |  |  |  |  |  |

**Step 2: Creating a Venn Diagram** (back of the page)

Draw a large box. Inside the box, write the name of the most general characteristic and the name of the organism that has ONLY that characteristic (Cells: Slugs). Continue creating boxes for the more specific traits using this same method. The largest box will represent the trait that is closest to the “root” of your cladogram.” The smallest box will represent the trait that is most specific (near the tip of one of your branches).

**Step 3: Draw Your Cladogram** (back of the page)

Note: each trait will represent a “tick mark” on the tree. Again, traits that are shared by most of the organisms will be shown by tick marks that are closer to the “root” of the cladogram